SEQUENCE LISTING

<110>   Seoul National University Industry Foundation

<120>   ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH
AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT

<130>   OP03-0015

<150>   KR 2003-19069
<151>   2003-03-27

<160>   9

<170>   KopatentIn 1.71

<210>   1
<211>   1089
<212>   DNA
<213>   Glycine max

<220>
<221>   CDS
<222>   (52)..(816)
<223>   Glycine max expansin (GmEXP1)

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atg ggc aaa atc atg ctt gtt ttg ggt agc ctc att gga tta tgc tgt   99
Met Gly Lys Ile Met Leu Val Leu Gly Ser Leu Ile Gly Leu Cys Cys
 1   5   10   15
ttc aca atc act acc tat gcc ttc tca cct tct gga tgg acc aac gcc   147
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
            20   25 ·   30
cat gcc act ttt tat ggg ggt agt gat gct tca gga act atg ggg gga   195
His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly
         35   40   45
gct tgt ggg tat ggg aat ctg tat gca act ggg tat gga act aga act   243
Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr
      50   55   60
gca gct tta agc act gcc tta ttt aat gat gga gct tcc tgt ggt cag   291
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln
65   70   75   80
tgc tac aaa att ata tgt gat tac aaa tca gac tct aga tgg tgc atc   339
Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile
                    85   90   95

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aaa gga aga tct  gta acc gta  act gcc aca aac  ttt  tgc cct  ccc aat   387
Lys Gly Arg Ser Val Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn
            100              105              110
ttc  gcc ctt  cct  aac aac aat  gga ggc tgg tgc aac  cca cca ctc  aag 435
Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Lys
        115              120              125
cat ttt  gat  atg gcc caa ccc gct tgg gaa aag att ggt att tac aga     483
His Phe Asp Met Ala Gln Pro Ala Trp Glu Lys Ile Gly Ile Tyr Arg
    130              135              140
gga ggg atc gtc ccc gtg cta  ttt caa  agg gtt cca tgc  aaa aag cat    531
Gly Gly Ile Val Pro Val Leu Phe Gln Arg Val Pro Cys Lys Lys His
145              150              155              160
gga ggg gtt agg  ttc agt  gtg aat ggg agg gac  tac ttt  gag cta  gta  579
Gly Gly Val Arg Phe Ser Val Asn Gly Arg Asp Tyr Phe Glu Leu Val
            165              170              175
ttg atc agc aat  gtg ggg ggt gct gga tcc atc caa tca gtg  ttc att     627
Leu Ile Ser Asn Val Gly Gly Ala Gly Ser Ile Gln Ser Val Phe Ile
            180              185              190
aaa ggc tca aaa  act gga tgg atg  gca atg  tca aga aat  tgg ggt tct    675
Lys Gly Ser Lys Thr Gly Trp Met Ala Met Ser Arg Asn Trp Gly Ser
        195              200              205
aat  tgg caa tcc  aat gcg tat  ttg  aat  ggt caa tct  ttg  tcc ttc  agg 723
Asn Trp Gln Ser Asn Ala Tyr Leu Asn Gly Gln Ser Leu Ser Phe Arg
    210              215              220
gtc acc  acc act  gat gga gag acc aga gtt  ttc  caa gat att gtt cca    771
Val Thr Thr Thr Asp Gly Glu Thr Arg Val Phe Gln Asp Ile Val Pro
225              230              235              240
gta agt  tgg aca ttc  ggc caa act  ttc  tct agc cca  gtt cag ttc  taag 820
Val Ser Trp Thr Phe Gly Gln Thr Phe Ser Ser Pro Val Gln Phe
            245              250              255
ctgattacag ataaaccaac caacggctga ggcgtgcttt tttattttat tactggagct     880
gcccgccacc cttcttctgg ttttgattat tcccatcaac tccaagccct ctatcaaggc     940
ataaattctt atcaataata caatcaatca ccatcatatc atcataagct tgtatatcaa     1000
ataaacatct ttcaagttta aattaattta tactataaat tgttgtaata tcattatagt     1060
tgaagttcaa aaaaaaaaaa aaaaaaaaa                                       1089


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<212>  PRT
<213>  Glycine max

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Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
            20              25              30
His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly
        35              40              45
Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr
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                50                    55                    60
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln
 65                    70                    75                    80
Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile
                    85                    90                    95
Lys Gly Arg Ser Val Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn
              100                   105                   110
Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Lys
          115                   120                   125
His Phe Asp Met Ala Gln Pro Ala Trp Glu Lys Ile Gly Ile Tyr Arg
      130                   135                   140
Gly Gly Ile Val Pro Val Leu Phe Gln Arg Val Pro Cys Lys Lys His
145                   150                   155                   160
Gly Gly Val Arg Phe Ser Val Asn Gly Arg Asp Tyr Phe Glu Leu Val
              165                   170                   175
Leu Ile Ser Asn Val Gly Gly Ala Gly Ser Ile Gln Ser Val Phe Ile
              180                   185                   190
Lys Gly Ser Lys Thr Gly Trp Met Ala Met Ser Arg Asn Trp Gly Ser
          195                   200                   205
Asn Trp Gln Ser Asn Ala Tyr Leu Asn Gly Gln Ser Leu Ser Phe Arg
      210                   215                   220
Val Thr Thr Thr Asp Gly Glu Thr Arg Val Phe Gln Asp Ile Val Pro
225                   230                   235                   240
Val Ser Trp Thr Phe Gly Gln Thr Phe Ser Ser Pro Val Gln Phe
              245                   250                   255
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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer

<400>   3
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<210>   4
<211>   37
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer

<400>   4

<210> 5
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

<400> 5
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tgytayaara thathtgyga ytayaarwsn gaywsnmgnt ggtgyathaa rggnmgnwsn 180
gtnacngtna cngcnacnaa yttytgyccn ccnaayttyg cnytnccnaa yaayaayggn 240
ggntggtgya ayccnccnyt naarcaytty gayatggcnc arccngcntg ggaraarath 300
ggnathtaym gnggnggnat hgtnccngtn ytnttycarm gngtnccntg yaaraarcay 360
ggnggngtnm gnttywsngt naayggnmgn gaytayttyg arytngtnyt nathwsnaay 420
gtnggnggng cnggnwsnat hcarwsngtn ttyathaarg gnwsnaarac nggntggatg 480
gcnatgwsnm gnaaytgggg nwsnaaytgg carwsnaay   519

<210> 6
<211> 269
<212> RNA
<213> Artificial Sequence

<220>
<223> RNA probe(antisense)

<400> 6
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gaacugggcu agagaaaguu uggccgaaug uccaacuuac uggaacaaua ucuuggaaaa 120
cucuggucuc uccaucagug guggugaccc ugaaggacaa agauugacca uucaaauacg 180
cauuggauug ccaauuagaa ccccaauuuc uugacauugc cauccaucca guuuuugagc 240
cuuuaaugaa cacugauugg auggaucca   269

<210> 7
<211> 389
<212> RNA
<213> Artificial Sequence

<220>
<223> RNA probe(sense)

<400> 7
uggauccauc caaucagugu ucauuaaagg cucaaaaacu ggauggaugg caaugucaag 60
aaauuggggu ucuaauuggc aauccaaugc guauuugaau ggucaaucuu uguccuucag 120
ggucaccacc acugauggag agaccagagu uuuccaagau auuguuccag uaaguuggac 180
auucggccaa acuuucucua gcccaguuca guucuaagcu gauuacagau aaaccaacca 240
acggcugagg cgugcuuuuu uauuuuauua cuggagcugc ccgccacccu ucuucugguu300
uugauuauuc ccaucaacuc caagcccucu aucaaggcau aaauucuuau caauaauaca 360
aucaaucacc aucauaucau cauaagcuu   389

<210>   8
<211>   28
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer

<400>   8
accaagcttc aacctctcat cattaggc   28

<210>   9
<211>   29
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer

<400>   9
accaagcttg gagttgatgg gaataatca   29